Practitioner's Docket No. 408445

Amendments to the Claims

1. (Currently Amended) A genetic construct for use in transforming cells, comprising:

a. a positive selectable marker gene that when transformed into the cells facilitates growth on a positive selective medium that is complementary to the positive selective marker gene,

b. a negative selectable marker gene that when rendered operable in the cells hinders growth on a negative selective medium that is complementary to the negative selectable marker, the negative selectable marker being different in kind from the positive selectable marker, and

c. two direct repeats of a gene of interest in a host cell, the direct repeats being effective for use in ~~which are capable of~~ recombination with the genome of the host cells, said direct repeats immediately flanking the positive and negative selectable marker genes of (a) and (b).

2. (Original) The genetic construct of claim 1 wherein the negative selectable marker gene is CodA.

3. (Original) The genetic construct of claim 2 wherein the positive selectable marker gene is NPTII, BAR, PAT or EPSP synthase

4. (Original) A method of removing selectable marker genes from transformed eukaryotic cells which comprises:

a. transforming cells with a genetic construct of claim 1,

b. culturing the cells of (a) on a positive selective medium,

c. transferring the transformed cells in (b) onto a negative selective medium, and

d. selecting the cells that grow on the negative selective medium wherein the selected cells that grow on the negative selective medium contain the gene sequence of interest but neither the positive selectable marker sequence nor the negative selectable marker sequence.

5. (Original) The method of claim 4 wherein the negative selectable marker gene is CodA.

6. (Original) The genetic construct of claim 1, wherein said construct comprises a polynucleotide sequence in the 5' to 3' (right to left) direction:

a. a gene sequence of interest,

b. a positive selectable marker sequence,

c. a negative selectable marker sequence and

d. a repeat of the gene sequence of interest in (a) above.

7. (Original) The genetic construct of claim 6 wherein the negative selectable marker sequence is CodA.

8. (Original) A method of removing selectable marker genes from transformed plant cells which comprises:

a. transforming cells with a genetic construct of claim 1 to form T0 transformants,

b. culturing the cells of (a) on a positive selective medium,

c. selecting the T0 transformant cells that grow on the positive selective medium,

d. regenerating a fertile T0 plant from the T0 transformant cells whereby T1 seed is formed,

e. collecting the T1 seed from the T0 plant or the seed from a subsequent Tn generation plant wherein n is a whole number greater than one,

f. germinating the T1 seeds or Tn seeds on a negative selective medium to form seedlings, and

g. selecting the seedlings that grow on the negative selective medium wherein the selected seedlings contain the gene sequence of interest but neither the positive selectable marker sequence nor the negative selectable marker sequence.

9. (Original) The method of claim 8 wherein the negative selectable marker gene is CodA and the negative selective medium comprises 5-fluorocytosine.

10. (Original) The genetic construct of claim 1, wherein said construct comprises, in the 5' to 3' direction (left to right), the formula:

GI-PS-NS-GI

wherein GI represents a gene of interest, PS represents a positive selectable marker gene and NS represents a negative selectable marker gene.

11. (Original) The genetic construct of claim 10 wherein NS is CodA.

12. (Original) The genetic construct of claim 1, wherein said construct comprises, in the 5' to 3' direction (left to right), the formula:

GI-NS-PS-GI

wherein GI represents a gene of interest, NS represents a negative selectable marker gene, and PS represents a positive selectable marker gene.

13. (Original) The genetic construct of claim 12 wherein NS is CodA.

14. (Original) The genetic construct of claim 1, wherein said construct comprises, in the 5' to 3' direction (left to right), the formula:

AGx-GI-PS-NS-GI-AG'y

wherein AG and AG' represent additional genes of interest, x represents an integer of 1 or larger, y represents an integer of 0 or larger, GI represents a gene of interest, NS represents a negative selectable marker gene, and PS represents a positive selectable marker gene.

15. (Original) The genetic construct of claim 14 wherein the genes represented by AG and AG' are never the same.

16. (Original) The genetic construct of claim 14 wherein the NS is CodA.

17. (Original) The method of claim 4 wherein the eukaryotic cell is a plant cell.

18. (Previously Presented) The method of claim 17 wherein the plant cell is a corn, soybean, cotton, wheat, canola, tobacco, Arabidopsis, rice, safflower or sunflower cell.

19. (Original) The method of claim 8 wherein the plant cell is a monocot or dicot cell.

20. (Previously Presented) The method of claim 19 wherein the plant cell is a corn, soybean, cotton, wheat, canola, tobacco, Arabidopsis, rice, safflower or sunflower cell.